

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: March 15, 2003, 15:07:49 ; Search time 74.0238 Seconds
(without alignments)
1537.035 Million cell updates/sec

Title: US-08-978-217-2

Perfect score: 1980
Sequence: 1 MATCEISNIFSNYSFAMYS.....YKFGKNSGCKEKEVLQSHN 371

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 segs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODE=frame_p2n.model -DEV=x1p
-Q=/cgn2_1/USPTO.spool/US08978217/runat_14032003_141838_13457/app_query.fasta_1.1500
-DB=Issued Patents NA -OPMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blomsun62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTMT=pct -NGRM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US08978217@cgn_1.1.131@runat_14032003_141838_13457 -NCPU=6 -ICPU=3
-NO XLPHY -NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA.*
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1980	100.0	1920	1	US-08-746-789A-1
2	559	28.2	5427	3	US-09-009-913-2
3	555.5	28.1	5510	3	US-09-009-913-3
4	555.5	28.1	5667	3	US-09-009-913-4
5	519.5	26.2	852	4	US-09-020-956-4
6	519.5	26.2	852	4	US-09-030-607-4
7	519.5	26.2	852	4	US-09-605-785-4
8	519.5	26.2	852	4	US-09-439-313-4
9	519.5	26.2	852	4	US-09-352-616A-4
10	519.5	26.2	852	4	US-09-232-149A-4
11	486.5	24.6	848	3	US-09-009-913-338
12	422	21.3	2280	3	US-09-009-913-8

13	422	21.3	2428	3	US-09-009-913-6	Sequence 6, Appl1
14	422	21.3	2498	3	US-09-009-913-10	Sequence 10, Appl1
15	246.5	12.4	2975	1	US-08-368-281-1	Sequence 1, Appl1
16	242	12.2	3240	1	US-08-368-281-3	Sequence 3, Appl1
17	238.5	12.0	1905	4	US-09-055-113-2	Sequence 2, Appl1
18	234.5	11.8	1752	4	US-09-360-779-1	Sequence 1, Appl1
19	234.5	11.8	1752	4	US-09-435-335-1	Sequence 1, Appl1
20	233	11.8	2268	3	US-09-344-579-1	Sequence 1, Appl1
21	228	11.5	1604	1	US-08-306-691B-43	Sequence 43, Appl1
22	228	11.5	1604	5	PCT-US93-06251-9	Sequence 9, Appl1
23	213.5	10.8	1528	4	US-08-878-177-3	Sequence 3, Appl1
24	212	10.7	2938	2	US-08-443-443B-3	Sequence 3, Appl1
25	207	10.5	1447	4	US-08-878-177-1	Sequence 1, Appl1
26	203.5	10.3	2266	2	US-09-213-767-1	Sequence 1, Appl1
27	190	9.6	2410	2	US-08-780-835B-1	Sequence 1, Appl1
28	190	9.6	2410	4	US-09-303-268-1	Sequence 1, Appl1
29	190	9.6	2410	4	US-09-116-049-1	Sequence 1, Appl1
30	189	9.5	2667	2	US-08-469-412A-1	Sequence 1, Appl1
31	189	9.5	2667	4	US-09-021-715-1	Sequence 1, Appl1
32	185.5	9.4	2064	3	US-08-875-944B-1	Sequence 1, Appl1
33	185.5	9.4	2064	4	US-09-116-049-3	Sequence 3, Appl1
34	158	8.0	1364	1	US-08-306-691B-50	Sequence 50, Appl1
35	158	8.0	1364	5	PCT-US93-06251-65	Sequence 65, Appl1
36	129	6.5	2544	2	US-08-469-412B-6	Sequence 6, Appl1
37	129	6.5	2544	4	US-09-021-715-6	Sequence 6, Appl1
38	109.5	5.5	1131	4	US-09-410-464-7	Sequence 7, Appl1
39	109.5	5.5	1308	4	US-09-410-464-6	Sequence 6, Appl1
40	101.5	5.1	3777	3	US-09-121-321-15	Sequence 15, Appl1
41	101.5	5.1	3777	4	US-08-933-803A-15	Sequence 15, Appl1
42	99.5	5.0	1640	3	US-09-330-095-2	Sequence 2, Appl1
43	99	5.0	2516	1	US-07-914-282D-2	Sequence 2, Appl1
44	99	5.0	2516	1	US-08-276-887A-2	Sequence 2, Appl1
45	99	5.0	2516	5	PCT-US93-02460-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-08-746-789A-1
; Sequence 1, Application US/08746789A
; Patent No. 5789200
; GENERAL INFORMATION:
; APPLICANT: Ismail Kola, Martin J. Tyms, Christine DeBouck
; TITLE OF INVENTION: A No. 5789200el Human ETS Family Member, ELR3
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road, P.O. Box 1539
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM 486
; OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
; SOFTWARE: MICROSOFT WORD
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/746,789A
; FILING DATE: No. 5789200el 15, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: William T. Han
; REGISTRATION/DOCKET NUMBER: 34,344
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610 270 5219
; TELEFAX: 610 270 4026
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 1920
 ; TYPE: Nucleic Acid
 ; STRANDEDNESS: Single
 ; TOPOLOGY: Linear
 ; ANTI-SENSE: No
 ; US-08-746-789A-1

Alignment Scores:
 Pred. No.: 3,676-186 Length: 1920
 Score: 1980.00 Matches: 371
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1 Gaps: 0

US-08-978-217-2 (1-371) x US-08-746-789A-1 (1-1920)

QY 1 MetalaalathrCysglulleseraniilepheserantyrpheseralametyrser 20
 Db 115 ATGCTGCAACCTGAGATTAGCAACATTTTACCACTTCACTGCGATGATGAC 174
 QY 21 SerGluappserThrleuAlaserValProProAlaAlaThrPhaglyAlaAspAspLeu 40
 Db 175 TCGAGGACTCCACCTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 234
 QY 41 ValLeuThrLeuSerAspProGlnmetSerLeuGluGlyThrGlyLeuAlaserTrpleu 60
 Db 225 GTACTGACCTTGACGACCAACCCAGATGATGAGAGGATGACAGAGGCTGCTG 294
 QY 61 GlyGluGlnProGlnPheTrpSerLystrGlnValLeuAspTrpLeuSerTrpGlnVal 80
 Db 295 GGGGAACAGCCCACTTGTGTCGAAGAGCAGGTTCTGATGATGATGATGATGATG 354
 QY 81 GluLyserLeuLystrAspAlaserAlaIleAspPheSerArgCysAspMetAspGlyAla 100
 Db 355 GAGGAAGAACATGATGACGACCAAGCCCATTTGACTCTCGATGATGATGATGATG 414
 QY 101 ThrLeuCysAsnCyAlaleuGluGluLeuValPheGlyProleuGlyAspGln 120
 Db 415 ACCCTCTGCATTTGCTTCCAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 474
 QY 121 LeuHlaIaGlnLeuArgAspLeuThrSerSerSerSerAspGlyLeuSerTrpIleIle 140
 Db 475 CTCCATGCCACCTGAGACCTCACTTCCAGCTCTTGATGATGATGATGATGATG 534
 QY 141 GluLeuLeuGluLyserGlyMetAlaPheGlnGluAlaLeuAspProGlyProPheAsp 160
 Db 535 GAGCTGCTGAGAAAGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 594
 QY 161 GlnGlySerProPheAlaGlnGluLeuLeuAspGlyGlnAlaIleAspProTrpHis 180
 Db 595 CAGGAGCAGCCCTTTGCCAGAGAGCTGCTGAGAGAGCTGAGAGAGAGAGAGAG 654
 QY 181 ProGlySerCysGlyAlaGlyAlaProSerProGlySerSerAspValSerThrAlaGly 200
 Db 655 CCCGAGAGCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 714
 QY 201 ThrGlyAlaSerArgSerSerHisSerSerAspSerGlyGlySerAspAlaAspLeuAsp 220
 Db 715 ACTGATGCTTCTCGAGAGCTCCCACTCTGAGACTCGGAGAGAGAGAGAGAGAG 774
 QY 221 ProThrAspGlyLyLeuLeuPheProSerAspGlyPheArgAspCysLyserGlyAspPro 240
 Db 775 CCCACTGATGAG 834
 QY 241 LyserHlaGlyLyserArgLyserArgLyserProArgLyserLeuSerLyserGlyTrpAspCys 260
 Db 835 AAGCAAGGAG 894
 QY 261 LeuGluGlyLyserLyserLyserHisAlaProArgGlyThrHisLeuTrpGluPheIleArg 280
 Db 895 CTGAGAGGAG 954

QY 281 AspIleLeuIleHisProGluLeuAsnGluGlyLeuMetLystrGluAsnArgHlaGlu 300
 Db 955 GACATCTCATCCACCCGAGAGCTCAACAGAGGCTCATGAAATGGGAGAAATCCGCATGAA 1014
 QY 301 GlyValPheLyserPheLeuArgSerGlyAlaValAlaGlnLeuTrpGlyGlnLyserLyser 320
 Db 1015 GCGCTTCAAGTTCTCGGCTCGAGGCTGTGGCCCACTATGGGGCAAAAGAAAAG 1074
 QY 321 AsnSerAsnMetThrTrpGlyGluLyserArgAlaMetArgTrpTrpLyserArgGlu 340
 Db 1075 AACGACAAATGACTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1134
 QY 341 IleLeuGluArgValAspGlyArgArgLeuValTrpLyserPheGlyLyserSerGly 360
 Db 1135 ATCTCGAAGCGGTGATGAGCGCGGAGACTCCTCTACAAAGTTGGCAAAACTCAAGCGGC 1194

QY 361 TrpLyserGluGluGlnValLeuGlnSerArgAsn 371

Db 1195 TGAAGAGAGAAAGAGTTCTCAGAGTCGGAAC 1227

RESULT 2

US-09-009-913-2

; Sequence 2, Application US/09009913

; Patent No. 6087485

; GENERAL INFORMATION:

; APPLICANT: Axis Pharmaceuticals, Inc.

; TITLE OF INVENTION: Asthma Related Genes

; NUMBER OF SEQUENCES: 339

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Bozicevic & Reed, LLP

; STREET: 285 Hamilton Ave, Suite 200

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94301

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/009,913

; FILING DATE: 21-JAN-1998

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; ATTORNEY/AGENT INFORMATION:

; NAME: Sherwood, Pamela J

; REGISTRATION NUMBER: 36,677

; REFERENCE/DOCKET NUMBER: SEQ-4P

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-327-3231

; TELEFAX: 650-327-3231

; TELEX:

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 5427 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

US-09-009-913-2

Alignment Scores:

Pred. No.: 4,586-45 Length: 5427
 Score: 559.00 Matches: 140
 Percent Similarity: 47.42% Conservative: 44
 Best Local Similarity: 36.08% Mismatches: 88
 Query Match: 28.23% Indels: 116
 DB: 3 Gaps: 12

US-08-978-217-2 (1-371) x US-09-009-913-2 (1-5427)

```

Qy 27 AlaserValProProalaaIaThr-----PheglYalaAspLeuValLeuThr 43
Db 84 GCGGCTCCCTCCATCAGACAGCATATTGATTTCCACCAGAAATCTTTAGSTA--- 140
Qy 44 LeuSerAsnProGlnMetSerLeuGluGly----- 53
Db 141 -----AATGATCATGATTTCTGAAAGAGTGATGTAATGAACTCAACCCCGCAAC 194
Qy 54 -----ThrglYalaAsp----- 58
Db 195 AACCTCCTTACACAGCCGCCAGCTGAGACAGACTACTCCAGTGCATGTTCCAGT 254
Qy 59 -----TripleGlyGluGlnProGlnPheTrpSerLeuThrGlnVal 72
Db 255 GGGTTTTTGGAGGCGCATGAGTAATTCATCTCTGATCTGACCAATGACAGGTG 314
Qy 73 LeuAspTrpIleSerLeuValGlnValGlnValAsnValAspAlaIleAspPhe 92
Db 315 TGGAGATGGCTCCACACCTCTGACACCAACAGCTGATGCAATTTGATCCCTTTC 374
Qy 93 SerArgCysAspMetAspGlyAlaThrLeuCysAsnValAlaLeuGluLeuArgLeu 112
Db 375 CAAGAGTTTCACATCAACGCGGACACCTCTGACAGCATGATTTGACAGAGTTACCCGG 434
Qy 113 ValPheGlyProLeuGlyAspGlnLeuHisAlaGlnLeuAspLeuThr----- 129
Db 435 GCGGACAGGAGCGGGGCGAGCTCTCTACAGCAACTTGCAGCATCTGAATGGAACGGC 494
Qy 130 SerSerSerSerAspGluLeuSerTrpIleIleGluLeuGluValAspGlyMetAla 149
Db 495 CAGTCAGTAGTGAC-----CTG 512
Qy 150 PheGlnGluAlaLeuAspProGlyProPheAspGlnGlySerProPheAlaGlnGluLeu 169
Db 513 TTCAGTCC-----ACACACAAATGTC 533
Qy 170 LeuAspAspGlyGlnGlnAlaSerProTrpHisProGlySerCysGlyAlaValPro 189
Db 534 ATTCTCAAGCTGAACAACTGAGCT----- 560
Qy 190 SerProGlySerSerAspValSerThrAlaGlyThrGlyAlaSerArgSerHisSer 209
Db 561 -----TCCATCATGAACCTGGAAGACGAGCACTTATATAT 599
Qy 210 SerAspSerGlyGlySerAspValAspLeuAspProThrAspGlyValLeuPheProSer 229
Db 600 GACACCAACTATGATGACAGTAGATTG-----TTGACAGCAAAACTTTC----- 647
Qy 230 AspGlyPheArgAspCysValLeu----- 237
Db 648 -----TGCCGGGCTCAGATCTCCATGACACACACGACCTTCTGTT 692
Qy 238 GlyAspProLysHisGlyLysArgLysArgLysArgProArgLysLeuSerLeuGlyTr 257
Db 693 GCAGAGTCACCTGATATGAAAAGAGCAAGACCCCTGCAAGTGCCACACAA--- 749
Qy 258 TrpAspCysLeuGluGlyLysLysSerLeuHisAlaProArgGlyThrHisLeuTrpGlu 277
Db 750 -----AAGCAAAACCGAGAGGACCTCATTTAGGAA 782
Qy 278 PheIleArgAspIleLeuIleHisProGluLeuAsnGluLysMetLeuTrpGluAsn 297
Db 783 TTCATTCGCGCATCTCTTGAACCCAGACAAAGAACCAAGATTTATATAATGGAGAC 842
Qy 298 ArgHisGluGlyValPheLysPheLeuArgSerGluAlaValAlaGlnLeuTrpGlyGln 317
Db 843 CGATCTGAGGGCGCTTCTCAGGTTCTGAATCAAGGACAGTGCGCTCAGCTATGGGTTAA 902
Qy 318 LysLysLysAsnSerAsnMetThrTrpGluLysLeuSerArgAlaMetArgTrpTrpTrp 337
Db 903 AAGAAGAACAAACAGCAGCATGACTATGAAAGCTCACCCAGAGCTATGAGATATTATAC 962

```

```

Qy 338 LysArgGluIleLeuGluArgValAspGlyArgArgLeuValTrpLysPheGlyLysAsn 357
Db 963 AAAAGAAAATACTGAGCGCTGTGATGAGCAAGACTGATATATAATTTGGAGAAAT 1022
Qy 358 SerSerGlyTrpLysGluGluGlu 365
Db 1023 GCCCGAGATGAGAGAAATGAA 1046

RESULT 3
US-09-009-913-3
; Sequence 3, Application US/09009913
; Patent No. 6087485
; GENERAL INFORMATION:
; APPLICANT: Axy's Pharmaceuticals, Inc.
; TITLE OF INVENTION: Asthma Related Genes
; NUMBER OF SEQUENCES: 339
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bozicevic & Reed, LLP
; STREET: 285 Hamilton Ave, Suite 200
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/009,913
; FILING DATE: 21-Jan-1998
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sherwood, Pamela J
; REGISTRATION NUMBER: 36,677
; REFERENCE/DOCKET NUMBER: SEQ-4P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-327-3231
; TELEFAX: 650-327-3231
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5510 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-009-913-3

Alignment Scores:
Pred. No.: 1.04e-44 Length: 5510
Score: 555.50 Matches: 126
Percent Similarity: 51.24% Conservative: 39
Best Local Similarity: 39.13% Mismatches: 78
Query Match: 28.06% Gaps: 79
DB: 3

US-08-978-217-2 (1-371) x US-09-009-913-3 (1-5510)
Qy 59 TrpLeuGlyGluGlnProGlnPheTrpSerLeuThrGlnValLeuAspTrpIleSerTr 78
Db 356 TGGCATGAATAATTCATCTCTCAGTACTGAGCAAGTACAGAGGTGGAGTGCTCAGCAC 415
Qy 79 GlnValGluLysAsnValTrpAspAlaSerAlaIleAspHisSerArgCysAspMetAsp 98
Db 416 CTCCTGACACCAACACGATGATGCAATTTGATCCCTTCCAAAGATTGACATCAAC 475
Qy 99 GlyAlaThrLeuCysAsnValAlaLeuGluGluLeuValPheGlyProLeuGly 118
Db 476 GCGAGCACCTCTGACAGCATGATTTCCAGAGATTTCACCCGGGCGGAGGACGCGGGG 535

```

```

Oy      AepGlnLeuH1sAlaGlnLeuAArgApleuThr-----SerSerSerSerApsGu 135
Db      536 CAGCTCCTCTACACCACTTGCACACACTGAAGTGAACCGCAAGTGCAGTGTATC--- 592
Oy      136 LeuSerTrpIleIleGluLeuLeuGluLysApsGlyMetAlaPheGlnGluAlaLeuAps 155
Db      593 -----CTGTTCACAGTCC----- 604
Oy      156 ProGlyProPheAapGlnGlySerProPheAlaGlnGluLeuLeuApsApsGlyGlnGln 175
Db      605 -----ACACACATGTCACTTGTCAAGACTGAACAA 634
Oy      176 AlaSerProTrpHisProGlySerCyGlyAlaGlyAlaProSerProGlySerSerAps 195
Db      635 ACTGAGCT----- 643
Oy      196 ValSerThrAlaGlyTrpGlyAlaSerAArgSerSerHisSerSerApsGlyGlySer 215
Db      644 ---TCCATCATGAAACACCTGGAAAGACGAACACTATTATTATGACACCAACTATGTAGC 700
Oy      216 ApsValAapPheAapProTrpHisGlyLysLeuPheProSerApsGlyPheArgApsCys 235
Db      701 ACAGTAGATTGG-----TTGACAGCAAAACTTTC-----TGC 733
Oy      236 LysLys-----GlyApsProLysHisGly 243
Db      734 CGCGCTCGATCTCATGACACACACAGTCACTTCTCTTGCACAGTCACTGTATATG 793
Oy      244 LysAArgLysAArgGlyAArgProAArgLysLeuSerLysGlyTrpTrpApsCyLeuGlnGly 263
Db      794 AAAAAAGAGCAAGACCCCTCGCCAAAGTCCACACCA----- 832
Oy      264 LysLysSerLysHisAlaProAArgGlyTrpHisLeuTrpGlnPheIleArgApsIleLeu 283
Db      833 -----AAGCAACAACCGAGAGGAGACTCACTTATGGAAATTCATCCGCAACATCCTC 883
Oy      284 IleHisProGlnLeuApsGlnGlyLeuMetLysGTrpGlnAsnAArgHisGlnGlyAlaPhe 303
Db      884 TTGAACCCACAGACAAAGAACCCAGCATTAATAATATGGGAAGACCGACTGAGGGCGCTTTC 943
Oy      304 LysPheLeuAArgSerGluAlaAlaAlaGlnLeuTrpGlyGlnLysLysLysApsSerAps 323
Db      944 AGGTCTTGAATATCAGAGGCAGTGGCTCAGCTATGGGGTAAAAAGAAACAACAGCAGC 1003
Oy      324 MetTrpTrpGlnLysLeuSerAArgAlaMetAArgTrpTrpTrpLysAArgGlnIleLeuGln 343
Db      1004 ATGACTTATGAAAAAGCTCAGCGCATGATGATTAATCAACAAAGAAATACTCGAG 1063
Oy      344 ArgValAapGlyAArgAArgLeuValTrpLysPheGlyLysApsSerSerGlyTrpLysGln 363
Db      1064 CGTGTGATGAGCAAGACGCTGTTATTAATTTGGGAAGATGCCGAGAGTGAAGAGA 1122
Oy      364 GluGln 365
Db      1124 AATGAA 1129

RESULT 4
US-05-009-913-4
; Sequence 4, Application US/0909913
; Patent No. 6087485
; GENERAL INFORMATION:
; APPLICANT: AxyS Pharmaceuticals, Inc.
; TITLE OF INVENTION: Aethna Related Genes
; NUMBER OF SEQUENCES: 339
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bozicevic & Reed, LLP
; STREET: 285 Hamilton Ave, Suite 200
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:

```

```

: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/009,913
: FILING DATE: 21-JAN-1998
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Sherwood, Pamela J
: REGISTRATION NUMBER: 36,677
: REFERENCE/DOCKET NUMBER: SEQ-4P
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650-327-3231
: TELEFAX: 650-327-3231
: TELEX:
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 5667 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: US-09-009-913-4

Alignment Scores:
Pred. No.: 1.08e-44 Length: 5667
Score: 555.50 Matches: 126
Percent Similarity: 51.24% Conservative: 39
Best Local Similarity: 39.13% Mismatches: 78
Query Match: 28.06% Indels: 79
DB: 3 Gaps: 8

US-08-978-217-2 (1-371) x US-09-009-913-4 (1-5667)

Qy 59 TrrpleuglyglnglnProglInpheTrrpserlyThrGlnValLeuaspTrrpIleserTyr 78
Db 513 TGGCATGAATTTCATCTCTCAGTACTGGACCAAGTACAGGTGTGGTGGCTTCAGAC 572
Qy 79 GlnValGlnlysaenlyrTYrAspAlaserAlaleapheserargyCysaapmetasp 98
Db 573 CTCCTGGACACCAACCAAGCTGGATGCCAATTGTATCCCTTCCAGAGTTGCACATCAAC 632
Qy 99 GlnAlaThrLeuCYsaenCYsaAlaleuGlnGlnLeuargLeuValPheGlyProLeuGly 118
Db 633 GCGCAGCACCTCTGACAGCATAGTTTGACAGAGTTCAACCCGGCGGAGGACGCGCGG 692
Qy 119 AspGlnLeuHIsalagInLeuargAspLeuThr-----SerSerSerSeraspGlu 135
Db 693 CAGCTCTCTACAGCACTTGACAGCATCTGAAAGTGAAGCAAGCGCCAGTGCATAGTAC--- 749
Qy 136 LeuSerTrrpIleIleGlnLeuLeuGlnLysAspGlyMetAlaPheGlnGlnAlaLeuasp 155
Db 750 -----CTGTTCCAGTCC----- 761
Qy 156 ProGlyProPheaspGlnGlySerProPheAlagInGlnLeuLeuaspAspGlyGlnGln 175
Db 762 -----ACACACAATGTCATTGTCACAGACTGAACAA 791
Qy 176 AlaSerProTYrHisProGlySerCYsGlyAlaGlyAlaProSerProGlySerSerasp 195
Db 792 ACTGAGCT----- 800
Qy 196 ValSerThrAlaGlyThrGlyAlaSerargSerSerHisSerSeraspSerGlyGlySer 215
Db 801 ---TCCATCATGACACCTGGAAGACGAGAACTATTATATGACACCAACTATGTGATGC 857
Qy 216 AspValaAspLeuaspProThrAspGlyLysLeuLeuPheProSeraspGlyPheAlaGaspCys 235
Db 858 ACAGTAAAGTTTG-----TTGGACGACGAAACCTTTC---TGC 890

```


Qy 356 LysAenSerSerGlyTrrpLysGluGlu 365
 Db 142 AAGAATGCCCGAGATGAGAGAAATGAA 113

RESULT 6
 US-09-030-607-44/C
 Sequence 44, Application US/09030607
 Patent No. 6262245
 GENERAL INFORMATION:
 APPLICANT: Xu, Jiangchun
 APPLICANT: Dillon, Davin C.
 TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
 NUMBER OF SEQUENCES: 224
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/030,607
 FILING DATE: 25-FEB-1998
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Makl, David J.
 REGISTRATION NUMBER: 31,392
 REFERENCE/DOCKET NUMBER: 210121.427C3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 44:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 852 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 US-09-030-607-44

Alignment Scores:
 Pred. No.: 2,296-42 Length: 852
 Score: 519.50 Matches: 121
 Percent Similarity: 50.97% Conservative: 37
 Best Local Similarity: 39.03% Mismatches: 73
 Query Match: 26.24% Indels: 79
 DB: 4 Gaps: 8

US-08-978-217-2 (1-371) x US-09-030-607-44 (1-852)

Qy 71 GlnValLeuAspTrpLysSerGlyGlnValGluLysAspLysLeuTyrAspLysAlaIle 90
 Db 850 CAGGTGTGGAGTGGCTCATGACCTCTGGACACCAACGAGTGGATGTTGTTATC 791

Qy 91 AspPheSerArgCysAspMetAspGlyAlaThrLeuCysAsnCysValLeuGluGluLeu 110
 Db 790 CCTTTCAGAGATGTGACATCAACGCGGACACCTTTGACAGATGAGTTTGCAGAGAGTTG 731

Qy 111 ArgLeuValPheGlyProLeuGlyAspGlnLeuHisAlaGlnLeuArgPheLeuThr 129
 Db 730 ACCCGGCGCGAGGAGCGCGGGGCGANCTCTCTACAGCAACTTGACGATCTGAAGTGG 671

Qy 130 -----SerSerSerSerArgGlyLeuSerTrpLysLeuLeuGluLeuGluLysAspGly 147
 Db 670 AACGGCACTGAGTAGTGAC----- 650

Qy 148 MetAlaPheGlnGluAlaLeuAspProGlyProPheAspGlnGlySerProPheAlaGln 167
 Db 649 ---CTGTTCCAGTCC-----ACACAC 632

Qy 168 GluLeuLeuAspAspGlyGlnGluAlaSerProTyrHisProGlySerCysGlyAlaGly 187
 Db 631 AATGTCATTGTCAGACTGACAACTAGACCT----- 599

Qy 188 AlaProSerProGlySerSerAspValSerThrAlaGlyThrGlyAlaSerArgSerSer 207
 Db 598 -----TCCATCATGAACACTGGAAAGACAGAACTAT 566

Qy 208 HisSerSerAspSerGlyGlySerAspValAspLeuAspProThrAspGlyLysLeuPhe 227
 Db 565 TTATATGACACCACTATGTAAGCAGTAAATTGG-----TTGACAGCAAAACTTTG 512

Qy 228 ProSerAspGlyPheArgAspCysLysLys----- 237
 Db 511 -----TCCGGGCTCAGATCTCCATGACAAACCACTACCTT 473

Qy 238 -----GlyAspProLysHisGlyLysArgLysArgGlyArgProArgLysLeuSerLys 255
 Db 472 CCTGTTGACAGATCACTGATATGAAAAAGAGCAAGACCCCTGCCAAGTCCACAC 413

Qy 256 GlyTyrTrpAspCysLeuGluGlyLysLysSerLysHisAlaProArgGlyThrHisLeu 275
 Db 412 AAA-----AAGCACAACCCGAGGGGACTCCTACTTA 383

Qy 276 TrpGluPheIleArgAspLysLeuLeuHisProGluLeuAsnGluGlyLeuMetLysTrp 295
 Db 382 TGGGAATTCATCCGACATCTCTTGAACCCAGCAAGAACCCGAGTTATATAAATGG 323

Qy 296 GluAsnArgHisGluGlyValPheLysPheLeuArgSerGlyAlaValAlaGlnLeuTrp 315
 Db 322 GAAGACCATTCGAGGGGCTTCAAGTTCTGAAATCAGAGGCGAGTGCCTAGCTATGG 263

Qy 316 GlyGlnLysLysLysAsnSerAsnMetThrTyrGlyLysLeuSerArgAlaMetArgLysTrp 335
 Db 262 GGTAAAAAGAGAACMACAGCGCATGACCTATGAAAAAGCTCAGCGGCTATGAGATAT 203

Qy 336 TyrTyrLysArgGlyLysLeuGluArgValAspGlyArgArgLeuValTyrLysPheGly 355
 Db 202 TACTACAAAAGAAATTCGTGAGCGGTGGAGTGAACAGACAGCTGTATATAAATTTGG 143

Qy 356 LysAenSerSerGlyTrrpLysGluGlu 365
 Db 142 AAGAATGCCCGAGATGAGAGAAATGAA 113

RESULT 7
 US-09-605-785-44/C
 Sequence 44, Application US/09605785
 Patent No. 6321716
 GENERAL INFORMATION:
 APPLICANT: Xu, Jiangchun
 APPLICANT: Dillon, Davin C.
 APPLICANT: Mitcham, Jennifer L.
 APPLICANT: Harlocker, Susan L.
 APPLICANT: Jiang, Yugu
 APPLICANT: Henderson, Robert A.
 APPLICANT: Kalos, Michael D.
 APPLICANT: Fanger, Gary R.
 APPLICANT: Retter, Marc W.
 APPLICANT: Stolk, John A.
 APPLICANT: Day, Craig H.
 APPLICANT: Vedrick, Thomas S.
 APPLICANT: Carter, Derrick
 APPLICANT: Li, Samuel
 APPLICANT: Wang, Aijun
 APPLICANT: Skeiky, Yasir A.W.
 APPLICANT: Hepler, William
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
 FILE REFERENCE: 210121.427C16

```

: CURRENT APPLICATION NUMBER: US/09/605,785
:
: CURRENT FILING DATE: 2000-06-27
:
: NUMBER OF SEQ ID NOS: 835
:
: SOFTWARE: FastSeq for Windows Version 3.0
:
: SEQ ID NO 44
:
: LENGTH: 852
:
: TYPE: DNA
:
: ORGANISM: Homo sapien
:
: FEATURE:
:
: NAME/KEY: misc feature
:
: LOCATION: (1)..(852)
:
: OTHER INFORMATION: n = A,T,C or G
:
: US-09-605-785-44

```

Alignment Scores:	
Pred. No.:	2,29e-42
Score:	519.970
Percent Similarity:	50.97%
Best Local Similarity:	39.03%
Query Match:	26.24%
DB:	4
	Gaps:
	8
	length:
	Matches:
	Conservative:
	Mismatches:
	Indels:
	Gaps:

US-08-978-217-2 (1-371) X US-09-605-785-44 (1-852)

Qy	71	GLNVALLLEuAAPTPIIleSeTyrGlnValIdIuYsbnIySTYrAaPAlaseAlaIle	90
Db	850	CAGGTGGGGAGTGGCTTCATCACTACTCTGGACCAACCAAGCTGGATGGCAATTGATTC	7921
Qy	91	AsPheSeTArGcYsAsPMeTAsPglYAlAlathrIuYcYsAnCYsAlAlaEugIuLeu	110
Db	790	CCTTTCCANNGATGTCGACATCAACGGGAGGACCTTTGGACGACATGATTTGGAGGATTC	7211
Qy	111	ArgLeuValPhegIYrProLeuGlyAspGlnLeuHiSalagIuLeuAArgPLeuThr--	129
Db	730	ACCCGGCGGAGGAGGACCGCGGGGCAMCTCTCTACAGCAACTTGCAGACATCTGAAGTGG	6711
Qy	130	-----SerSerSerAsPgluSeuSerTrIleIleGluLeuLeuGluYsAsPgly	147
Db	670	AACGGCCAGTCAGAGTATGAC-----	650
Qy	148	MetAlaPheGIngluAlAlaLeuAsPProGlyrProPheAsPInglIySerProPheAlaGln	167
Db	649	---CTGTTCAGTCC-----ACACAC	632
Qy	168	GluLeuLeuAsPAsPglYgInGlnAlaIasePProGlyrHiSProGlySerCysGlyAlaGly	187
Db	631	AATGTCATTGTCAAGACTGACAAACATGAGCT-----	599
Qy	188	AlaPAsPAsPProGlySerSerAsPValSerThrAlaGlyThrGlyAlaIasePAsPSer	207
Db	598	-----TCCATTCATGAACACTGATCGAAGACCAACCACTAT	566
Qy	208	HisSerSerAsPAsPglYgIYSerAsPValAlaSerLeuAsPProThrAsPAlYlyLeuPhe	227
Db	565	TTATATGACACCAACCTATGATGATGACAGCATGATGATTTG-----TTGGACAGCAAAACTTTC	512
Qy	228	ProSeTAsPAsPglYrPheArgAsPcYsLeuYs-----	237
Db	511	-----TGCCGGGCTCAGATCTCCATGACAAACACCAGTCACTT	473
Qy	238	-----GluAsPProLYsHiGlyLYsAlaGlyLYsAlaGlyArgLYsProAlaGlyLeuSerLYs	255
Db	472	CCTGTTCGACAGTCACTCGATATGAAAAGAGCAACAGCCCTCTGCCAAGTGGCCACACC	413
Qy	256	GluYrYrTrPAsPAsPglYgIYLYsLYsSerLYsHiSalAProAlaGlyLYrThiHiLeu	275
Db	412	AAA-----AAGCAACAACCCGAGGGGACTCACTTA	383
Qy	276	TrpGluPheIleArgAsPAlaLeuIleHisPProGluLeuAsnGluGlyLeuMetLYsTrp	295
Db	382	TGGGAATTCAATCCGGAGCATCTCTTGAAACCCAGACAAAGAACCCAGGATTTATATAAATGG	323
Qy	296	GluAsnArgHISgluGlyValPheIySerPheLeuArgSerGluAlaValAlaGlnLeuTrp	315

Dd	322	GAGAGCCGATCTGAGGGCGTTTAAAGGTTCTTGAAATCAGAGCGATGGCTCAGCTATGG	265
Qy	316	GlyGluValLysLysAsnSerAsnMetThrTyrgLulLysLeuSerAlaIleMetArgTyr	335
Dd	262	GGTAAAGAAAGAAACACAGCAGCATGCTCTATATAAAAGCTCAGCCAGCATATAGATAT	203
Qy	336	TyrTyrLysArgGluIleLeuGluArgValAspLysArgArgLeuValTyrLysPheGly	355
Dd	202	TACTACAAAAGAAATTTCTGGACCGCTGTGGATGGACGAGACTGTATATTAATTTGGG	143
Qy	356	LysAsnSerSerGlyTyrPylGluGluGlu	365
Dd	142	AAGATGCCCCAGAGATGGAGAGAAATGAA	113

RESULT 8

US-09-439-313-44/c
Sequence 44 Application US/09439313

```

Sequence 44, Application US/094319313
Patent No. 6329505

GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang Yugu
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael
APPLICANT: Fanger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.42769
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 44
LENGTH: 852
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(852)
OTHER INFORMATION: n = A,T,C or G
US-09-439-313-44

```

Alignment Scores:

Pred. No.:	2.29e-42	length:	853
Score:	519.50	Matches:	121
Percent Similarity:	50.97%	Conservative:	37
Best Local Similarity:	39.03%	Mismatches:	73
Query Match:	26.24%	Indels:	26
DB:	4	Gaps:	8

US-08-978-217-2 (1-371) x US-09-439-313-44 (1-852)

```

QY 71 GlnValLeuAspTrpLleSerTyrClnValcIuLulysAsnYsTrYrAspAlaSerAlaIle 90
Db 850 CAGTGTGGAGGTGGCTTCATCACTCTGGACCAACCAACGTGGATGCCAATTGTATC 79
QY 91 AepPheSerArgCyAspMetAspGlyValThrLeuCyAsnCySalAlaGluGluLeu 110
Db 790 CCTTTCCANAGATTCGACATCAACGGCGAGACCTTTTCACACATGAGATTCAGAGATTC 73
QY 111 ArgLeuValPheGlyProLeuGlyAspGluLeuHisAlaGluLeuValAspLeuThr-- 120
Db 730 AACCGGGGGGAGGAGCGCGGGGCANCTCCTTACAGCAACTTCGAGCATCTGAAGTGG 67
QY 130 -----SerSerSerSerAspGluLeuSerTrpLleIleGluLeuLeuGluLysAspGly 14
Db 670 AACGGCCAGTCGAGTAGTAC----- 65

```

```

Qy 148 MetAlaPheGlnGlnAlaLeuAspProGlyProPheAspGlnGlySerProPheAlaGln 167
Db 649 ---CTGTTCCAGTCC-----ACACAC 632
Qy 168 GluLeuLeuAspAspGlyGlnGlnAlaSerProTyrHisProGlySerCysGlyAlaGly 187
Db 631 AATGTCATTGTCAGACTGACAGCAACTGAGCCT----- 599
Qy 188 AlaProSerProGlySerSerAspValSerThrAlaGlyThrGlyValaSerSerSer 207
Db 598 -----TCCATCATGACAACCTCGAAAGACAGAACTAT 566
Qy 208 HisSerSerAspSerGlyGlySerAspValAspLeuAspProThrAspGlyTyrLeuPhe 227
Db 565 TTATATGACACCACTATGATGACACAGATTTG-----TTGACACGCAAACTTTC 512
Qy 228 ProSerAspGlyPheArgAspCysLeuValys----- 237
Db 511 -----TCCGGGCTCAGATCTCCATGACAACCAACGATCACTT 473
Qy 238 -----GlyAspProLysHisGlyLysArgLysArgGlyArgProArgLysLeuSerLys 255
Db 472 CCTGTTGCAAGATCACTGATATGAAAGAGCAAGACCCCTCGCAAGTCCACAC 413
Qy 256 GluTyrTTPAspCysLeuGlnGlyLysLysSerLysHisAlaProArgGlyThrHisLeu 275
Db 412 AAA-----AAGCAACAACCGAGAGGACTCACTTA 383
Qy 276 TTPGluPheIleArgAspIleLeuIleHisProGluLeuAspGlnGlyLeuMetLysTTP 295
Db 382 TGGGAATTCATCCGGACATCTCTTGAACCCAGACACACCCAGGATTAATAAATGG 323
Qy 296 GluAsnArgHisGlnGlyValPheLysPheLeuArgSerGlyAlaValAlaGlnLeuTTP 315
Db 322 GAAGCCCATCTGAGGGCTCTTCAAGTTCTTGAATCAGAGGCACTGCTACGTATGG 263
Qy 316 GlnGlnLysLysLysAsnSerAsnMetThrTyrGlnLysLeuSerArgAlaMetArgTyr 335
Db 262 GGTAAAAAGAAAGAACACAGCAGCATGACCTATGAAAGACTCAGCGACCTATGAGATTT 203
Qy 336 TyrTyrLysArgGlnIleLeuGlnLysValAspGlyArgArgLeuValTyrLysPheGly 355
Db 202 TACTCAAAAGAAATTCGTGAGCGGTGTGATGACGAAGACTGGTATATTAATTTGGG 143
Qy 356 LysAsnSerSerGlyTTPArgGlnGln 365
Db 142 AAGAAATGCCCGAGATGAGAGAAATGAA 113

RESULT 9
US-09-352-616A-44/c
: Sequence 44, Application US/09352616A
: Patent No. 6195278
: GENERAL INFORMATION:
: APPLICANT: Dillon, Davin C.
: APPLICANT: Harlocker, Susan Louise
: APPLICANT: Jiang, Yugu
: APPLICANT: Xu, Jiangchun
: APPLICANT: Mitcham, Jennifer Lynn
: TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
: FILE REFERENCE: 210121.427C8
: CURRENT APPLICATION NUMBER: US/09/352,616A
: CURRENT FILING DATE: 1999-07-13
: NUMBER OF SEQ ID NOS: 472
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO 44
: LENGTH: 852
: TYPE: DNA
: ORGANISM: Homo sapien
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)...(852)

```

```

: OTHER INFORMATION: n = A,T,C or G
US-09-352-616A-44
Alignment Scores:
Pred. No.: 2,29e-42 Length: 852
Score: 519.50 Matches: 121
Percent Similarity: 50.97% Conservative: 37
Best Local Similarity: 39.03% Mismatches: 73
Query Match: 26.24% Indels: 79
DB: 4 Gaps: 8

US-08-978-217-2 (1-371) x US-09-352-616A-44 (1-852)
Qy 71 GlnValLeuAspTTPIleSerTyrGlnValGlnLysAsnLysTyrAspAlaSerAlaIle 90
Db 850 CAGGTGTGAGATGGCTCATCATCACTCTGACACCAACCAAGCTGATGATGATATC 791
Qy 91 AspPheSerArgCysAspMetAspGlyAlaThrLeuCysAsnGlyValLeuGlnGlnLeu 110
Db 790 CCTTTCANAGATTGACATCAACCGCGAGCACTTTGACACATGATTTGCAGAGATTTC 731
Qy 111 ArgLeuValPheGlyProLeuGlyAspGlnLeuHisAlaGlnLeuArgAspLeuThr--- 129
Db 730 ACCCGGGCGGCAAGGACCGGGGGCANCTCTCTACAGCAACTTCACACATCTGAAGTGG 671
Qy 130 -----SerSerSerSerAspGlnLeuSerTTPIleIleGlnLeuGlnLysAspGly 147
Db 670 AACGGCCAGTGCAGTAGTGAC----- 650
Qy 148 MetAlaPheGlnGlnAlaLeuAspProGlyProPheAspGlnGlySerProPheAlaGln 167
Db 649 ---CTGTTCCAGTCC-----ACACAC 632
Qy 168 GluLeuLeuAspAspGlyGlnGlnAlaSerProTyrHisProGlySerCysGlyAlaGly 187
Db 631 AATGTCATTGTCAGACTGACAGCAACTGAGCCT----- 599
Qy 188 AlaProSerProGlySerSerAspValSerThrAlaGlyThrGlyValaSerArgSerSer 207
Db 598 -----TCCATCATGACAACCTCGAAAGACAGAACTAT 566
Qy 208 HisSerSerAspSerGlyGlySerAspValAspLeuAspProThrAspGlyLysLeuPhe 227
Db 565 TTATATGACACCACTATGATGACACAGATTTG-----TTGACACGCAAACTTTC 512
Qy 228 ProSerAspGlyPheArgAspCysLeuValys----- 237
Db 511 -----TCCGGGCTCAGATCTCCATGACAACCAACGATCACTT 473
Qy 238 -----GlyAspProLysHisGlyLysArgLysArgGlyArgProArgLysLeuSerLys 255
Db 472 CCTGTTGCAAGTCACTGATATGAAAGAGCAAGACCCCTCGCAAGTCCACAC 413
Qy 256 GluTyrTTPAspCysLeuGlnGlyLysLysSerLysHisAlaProArgGlyThrHisLeu 275
Db 412 AAA-----AAGCAACAACCGAGAGGACTCACTTA 383
Qy 276 TTPGluPheIleArgAspIleLeuIleHisProGluLeuAspGlnGlyLeuMetLysTTP 295
Db 382 TGGGAATTCATCCGGACATCTCTTGAACCCAGACACCAACGAGATTAATAAATGG 323
Qy 296 GluAsnArgHisGlnGlyValPheLysPheLeuArgSerGlyAlaValAlaGlnLeuTTP 315
Db 322 GAAGCCCATCTGAGGGGCTCTTCAAGTTCTTGAATCAGAGGCACTGCTACGTATGG 263
Qy 316 GlnGlnLysLysLysAsnSerAsnMetThrTyrGlnLysLeuSerArgAlaMetArgTyr 335
Db 262 GGTAAAAAGAAAGAACACAGCAGCATGACCTATGAAAGCTCAGCGGCTATGAGATAT 203
Qy 336 TyrTyrLysArgGlnIleLeuGlnLysValAspGlyArgArgLeuValTyrLysPheGly 355
Db 202 TACTCAAAAGAAATTCGTGAGCGGTGTGATGACGAAGACTGGTATATTAATTTGGG 143

```



```

Qy 356 LysAsnSerSerGlyTyrPlyGluGlu 365
Db 142 AAGAATGCCGAGATGAGAGAAAATGAA 113

RESULT 10
US-09-232-149A-44/C
Sequence 44, Application US/09232149A
Patent No. 6465611
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
FILE REFERENCE: 210121.427C6
CURRENT APPLICATION NUMBER: US/09/232,149A
CURRENT FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 338
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 44
LENGTH: 852
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(852)
OTHER INFORMATION: n = A,T,C or G
US-09-232-149A-44

Alignment Scores:
Pred. No.: 2,29e-42 Length: 852
Score: 519.50 Matches: 121
Percent Similarity: 50.97% Conservative: 37
Best Local Similarity: 39.03% Mismatches: 73
Query Match: 26.24% Indels: 79
Gaps: 8
DB:

US-08-978-217-2 (1-371) x US-09-232-149A-44 (1-852)
Qy 71 GlnValLeuAspTyrPleSerTyrGlnValGluLysAsnLysTyrAspAlaSerAlaIle 90
Db 850 CAGGTGGGAGTGAGTGCCTCCTCCTGAGACCAACGAGCTGAGCCAACTGTTATC 791
Qy 91 AspPheSerArgCysAspMetAspGlyValThrLeuCysAsnCysAlaLeuGluLys 110
Db 790 CTTTCCANGAGTTGAGATCAACGCGACGACCTTTGACAGATGAGTTGACAGAGTTC 731
Qy 111 ArgLeuValPheGlyProLeuGlyAspGlnLeuHisAlaGlnLeuArgAspLeuThr 129
Db 730 ACCGGGGCGGAGGAGCGGGGGCANCTCCTCTACAGCACTTGACAGATCTGAAGTGG 671
Qy 130 -----SerSerSerSerAspGluLeuSerTrpIleIleGluLeuGluLysAspGly 147
Db 670 AACGGCCAGTGCAGTAGTGC----- 650
Qy 148 MetAlaPheGlnGlnAlaLeuAspProGlyProPheAspGlnGlySerProPheAlaGln 167
Db 649 ---CTGTTCCAGTCC-----ACACAC 632
Qy 168 GluLeuLeuAspAspGlyGlnGlnAlaSerProTyrHisProGlySerCysGlyValaGly 187
Db 631 AATGTCATGTCAGACATCGAACAACAGCT----- 599
Qy 188 AlaProSerProGlySerSerSerAspValSerThrAlaGlyThrGlyAlaSerArgSerSer 207
Db 598 -----TCCATCATGAACCTCGAAGAGACAGACAGACATAT 566
Qy 208 HisSerSerAspSerGlyGlySerAspValAspLeuAspProThrAspGlyLysLeuPhe 227
Db 565 TTATATGACACCAACTATGATGACAGAGATTTG-----TTGACAGCAAAACTTTC 512
Qy 228 ProSerAspGlyPheArgAspCysLysLys----- 237

```

```

Db 511 -----TGCCGGGCTCAGATCTCCATGACACACACAGTACCTT 473
Qy 238 -----GlyAspProLysHisGlyLysArgLysArgGlyValArgProArgLysLeuSerLys 255
Db 472 CCGTTTCAGAGTCACCTGATATGAAAAAGAGCAAGACACCCCTGCGCAAGTGCCACACC 413
Qy 256 GluTyrTrpAspCysLeuGluGlyLysLysSerLysHisAlaProAlaGlyThrHisLeu 275
Db 412 AAA-----AAGCACAAACCGAGAGGAGTACCTTA 383
Qy 276 TrpGluPheIleArgAspIleLeuIleHisProGluLeuAsnGluGlyLysMetLysTrp 295
Db 382 TGGGAATTCATCCGCGACATCTTTCACCCAGACAAACCCAGGATTTATATAATGG 323
Qy 296 GluAsnArgHisGluGlyValAlaPheLysPheLeuArgSerGlnAlaValAlaGlnLeuTrp 315
Db 322 GAAGACCGATCTAGGGCGCTTCAGGTTCTTGAAATCAGAGGAGTGGCTCAGCTATGG 263
Qy 316 GlyGlnLysLysLysAsnSerAsnMetThrTyrGluLysLeuSerArgAlaMetArgTyr 335
Db 262 GGTAAAAAGAAACACACAGCATGACCTATGAAAAAGCTCAGCCGAGCTATGAGATAT 203
Qy 336 TyrTyrLysArgGluIleLeuGluArgValAspGlyValArgLeuValTyrLysPheGly 355
Db 202 TACTACAAAAGAGAAATTCGAGCGTGTGAGTGAAGACGAAAGACTGTATATAATTTGGG 143
Qy 356 LysAsnSerSerGlyTyrPlyGluGlu 365
Db 142 AAGAATGCCGAGATGAGAGAAAATGAA 113

RESULT 11
US-09-009-913-338
Sequence 338, Application US/09009913
Patent No. 6087485
GENERAL INFORMATION:
APPLICANT: Axy's Pharmaceuticals, Inc.
TITLE OF INVENTION: Asthma Related Genes
NUMBER OF SEQUENCES: 339
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bozicevic & Reed, LLP
STREET: 285 Hamilton Ave, Suite 200
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: IBM Compatible
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,913
FILING DATE: 21-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: SEQ-4P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-327-3231
TELEFAX: 650-327-3231
TELEX:
INFORMATION FOR SEQ ID NO: 338:
SEQUENCE CHARACTERISTICS:
LENGTH: 848 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:

```

```

; NAME/KEY: Coding Sequence
; LOCATION: 1...848
; OTHER INFORMATION:
US-09-009-913-338

Alignment Scores:
Pred. No.: 4,15e-39 Length: 848
Score: 486.50 Matches: 109
Percent Similarity: 51.53% Conservative: 43
Best Local Similarity: 36.95% Mismatches: 88
Query Match: 24.57% Indels: 55
DB: Gaps: 5

US-08-978-217-2 (1-371) x US-09-009-913-338 (1-848)
QY 57 AAlaserTLeuGluInProGlnPheTyrSerLeuThGlnValLeuAspTrpIle 76
DB 118 ACCCAGTGGCATGAAATCCACCTCAGTACTGAGCCAAATACCGAGTGGGAATGGCTG 177
QY 77 SerTyrGlnValGluYAsnLysTyrAspAlaSerAlaIleAspPheSerArgCysAsp 96
DB 178 CAGCACCTCTGACACCAACCTGACAGACGCTGAGCTGATCCCTTCCAGAGATTCGAC 237
QY 97 MetAspGlyAlaThrLeuCysAsnCysAlaLeuGluGluLeuArgValPheGlyPro 116
DB 238 ATTACGGGAGAACACCTGACAGATGAGCTGACAGAGTTCCAGAGGCGACAGGCTCA 297
QY 117 LeuGlyAspGlnLeuHisAlaGlnLeuArgAspLeuThr-----SerSerSer 133
DB 298 GCTGGGACACTCTCTACACCACTTACAGCATCTCAAGTGAAACGGCCAATGCACT 357
QY 134 AspGluLeuSerTrpIleIleGluLeuGluYAspGlyMetAlaPheGlnGlnAla 153
DB 358 GACCTTTTCCAGTCCGACACACATGCTATTGTCAAG-----ACTGAACA 402
QY 154 LeuAspProGlyProPheAspGlnGlySerProPheAlaGlnGluLeuAspGly 173
DB 403 ACCGATCCT-----TCCATCATGACACATG 429
QY 174 GlnGlnAlaSerProTyrHisProGlySerCysGlyAlaGlyAlaProSerProGlySer 193
DB 430 AAGAAGAAATATCTCTATGATCCAGTATGATGATGAGACAGTACATGTTGGACAG 489
QY 194 SerAspValSerThrAlaGlyThrGlyAlaSerArgSerSerHisSerSerAspSery 213
DB 490 AAGACTTTTCCCGGCTCAGATCTCAGTACGACAACCTCCAGTACTTCCAGTTGACAG 549
QY 214 GlySerAspValAspLeuAspProThrAspGlyLysLeuPheProSerAspGlyPheArg 233
DB 550 TCACCTGATATG----- 561
QY 234 AspCysLysLysLysAspProLysHisGlyLysArgLysLysArgGlyArgProArgLys 253
DB 562 -----AAAAAGAGCAAGACCACTT----- 582
QY 254 SerLysGluTyrTrpAspCysLeuGluGlyLysLysSerLysHisAlaProArgGlyThr 273
DB 583 -----GTAAGTCCCAACCAAAAAAGACAACCAAGGAGCACT 621
QY 274 HisLeuTyrGlnPheIleArgAspIleLeuIleHisProGluLeuAsnGluGlyLeuMet 293
DB 622 CACTTATGGAGATTCAATCCGAGACATTTCTTGAAGCCAGACAAGAACCCAGGGCTGATC 681
QY 294 LysTyrGlnAsnArgHisGlyGlyValPheLysPheLeuArgSerGlyAlaValAlaGln 313
DB 682 AATATGGAAGACGTTCCGAAAGCATCTTCAGGTTCTGTGAAGTCAAGAGCTGTGGCTCAG 741
QY 314 LeuTyrGlnGlnLysLysAsnSerAsnMetThrTyrGluLysLysSerArgAlaMet 333
DB 742 CTGTGGGGGAAAGAAATATACATGATACATACAGAAAGCTCAGCCGGGCTATG 801
QY 334 ArgTyrTyrTyrLysArgGluLeuGluArgValAspGlyArg 348

```

```

DB 802 AGATATTACTACAAACGAGAAATCTGGAACGTGTGATGACGA 846

RESULT 12
US-09-009-913-8
; Sequence 8, Application US/09009913
; Patent No. 6087485
; GENERAL INFORMATION:
; APPLICANT: Ays Pharmaceuticals, Inc.
; TITLE OF INVENTION: Aschna Related Genes
; NUMBER OF SEQUENCES: 339
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bozicevic & Reed, LLP
; STREET: 285 Hamilton Ave, Suite 200
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE: 21-JAN-1998
; APPLICATION NUMBER: US/09/009,913
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sherwood, Pamela J
; REGISTRATION NUMBER: 36,677
; REFERENCE/DOCKET NUMBER: SEQ-4P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-327-3231
; TELEFAX: 650-327-3231
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2280 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-09-009-913-8

Alignment Scores:
Pred. No.: 4,31e-32 Length: 2280
Score: 422.00 Matches: 90
Percent Similarity: 45.45% Conservative: 50
Best Local Similarity: 29.22% Mismatches: 70
Query Match: 21.31% Indels: 98
DB: Gaps: 5

US-08-978-217-2 (1-371) x US-09-009-913-8 (1-2280)
QY 59 TrpLeuGluGluGlnProGlnPheTyrSerLysThrGlnValLeuAspTrpIleSerTyr 78
DB 206 TGGACATCAGTCCACCTGAAATCTGAGTAAGCCCATGTGTGGAGAGGCTCCAGTTC 265
QY 79 GlnValGluYAsnLysTyrAspAlaSerAlaIleAspPheSerArgCysAspMetAsp 98
DB 266 TGGTGGACAGTACAAAGTTGAGACCAATTCATCTCTGCAACTTCAACATCAGT 325
QY 99 GlyAlaThrLeuCysAsnCysAlaLeuGluGluLeuArgLeuValPheGlyProLeuGly 118
DB 326 GGCCTGACAGCTGTGACAGATGACACAGAGGAGTTCTGAGAGCACTGGCTTGGCGGC 385
QY 119 AspGlnLeuHisAlaGlnLeuArgAspLeuThrSerSerSerAspGluLeuSerTrp 138
DB 386 GAGTACCTGTACTTATCTCCAAACATCCGACA----- 421
QY 139 IleIleGluLeuGluYAspGlyMetAlaPheGlnGlnAlaLeuAspProGlyPro 158

```

Db 421 ----- 421
 Qy 159 PheapngllyserProPhealaglIngluleuAaspGlyglInglInalaserPro 178
 Db 422 -----CAAGTTACTCTTTTAAATGACCGCTGAAGAAAGCAAGCCACCATCAAGAC 475
 Qy 179 TyrHisProGlyserCyGlyAlaGlyAlaProSerProGlySerSerAspValSerThr 198
 Db 476 TATCGTATTCACACTGC-----TTGAANAACA 502
 Qy 199 AlaGlyThrGlyAlaSerArgSerSerHisSerSerAspSerGlyGlySerAspValasp 218
 Db 503 AGTGCATC--AAAGTCAGACTGTACAGT----- 532
 Qy 219 LeuAspProThrAspGlyLysLeuPheProSerAspGlyPheArgAspCysLysGly 238
 Db 532 ----- 532
 Qy 239 AspProLysHisGlyLysArgLysArgGlyArgProArgLysLeuSerLysGlyTrp 258
 Db 532 ----- 532
 Qy 259 AspCysLeuGluGlyLysLysSerLysHisAlaProArgGlyThrHisLeuTrpGluPhe 278
 Db 533 -----CATAGTAGAACAAAGCCCTCCAAAGTTCTCATGTAGGAATTT 574
 Qy 279 IleArgAspIleLeuIleHisProGluLeuAsnGluGlyLeuMetLysTrpGluAsnArg 298
 Db 575 GTAGAGACCTGGCTTCTATCTCTGAAGAAAGCTGGCATTTCTGAATGGGAAGATGG 634
 Qy 299 HisGluGlyAlaPheLysPheLeuArgSerGluAlaValAlaGluLeuTrpGlyGlnLys 318
 Db 635 GAACAGGAATTTTCCGGCTGTAAATCGAAGCCCTGGCAAGATGTGGGCAAGAC 694
 Qy 319 LysLysAsnSerAsnMetThrTyGlyLysLeuSerArgAlaMetArgTyTrpLys 338
 Db 695 AAGAAAATGACAGAAATGACGTATGAAGATTGACAGAGCCCTGAGATCTACTATAA 754
 Qy 339 ArgGluIleLeuGluArgValAspGlyArgArgLeuValTyTrpLysPheGlyLysAsnSer 358
 Db 755 ACAGGAATTTTGGAGCGGGTGGAC--CGAAGTTAGTGTCAATTTGAAAAAATGCA 811
 Qy 359 SerGlyTrpLysGluGluGluVal 366
 Db 812 CACGGGTGCGAGAACAACTA 835
 RESULT 13
 US-09-009-913-6
 ; Sequence 6, Application US/09009913
 ; Patent No. 6087485
 ; GENERAL INFORMATION:
 ; APPLICANT: Axy's Pharmaceuticals, Inc.
 ; TITLE OF INVENTION: Asthma Related Genes
 ; NUMBER OF SEQUENCES: 339
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Bozicevic & Reed, LLP
 ; STREET: 285 Hamilton Ave, Suite 200
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94301
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/009,913
 ; FILING DATE: 21-JAN-1998
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:

; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Sherwood, Pamela J
 ; REGISTRATION NUMBER: 36,677
 ; REFERENCE/DOCKET NUMBER: SEQ-4P
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650-327-3231
 ; TELEFAX: 650-327-3231
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2428 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; US-09-009-913-6
 Alignment Scores:
 Pred. No.: 4.74e-32 Length: 2428
 Score: 422.00 Matches: 90
 Percent Similarity: 45.45% Conservative: 50
 Best Local Similarity: 29.22% Mismatches: 70
 Query Match: 21.31% Indels: 98
 DB: 3 Gaps: 5
 US-08-978-217-2 (1-371) x US-09-009-913-6 (1-2428)
 Qy 59 TrpLeuGlyGluGlnProGlnPheTrpSerLysThrGlnValLeuAspTrpIleSerTrp 78
 Db 354 TGACATCACTCCACCTGAATCTGACTGAAGGCGCATGTGGAGTGGCTCCAGTTC 413
 Qy 79 GlnValGlyLysAsnLysTyArgAlaSerAlaIleAspPheSerArgCysAspMetAsp 98
 Db 414 TGTCCGACCACTACAAAGTTGGACACCAATTCATCTCTTCTGCACTTCAATCAATCAGT 473
 Qy 99 GlyAlaThrLeuCyAsnCysAlaLeuGluGluLeuArgLeuValPheGlyProLeuGly 118
 Db 474 GGCTGACGCTGTCCAGCATGACACAGAGAGATTGTCGAGCAGCTGGCTCTGCGGC 533
 Qy 119 AspGlnLeuHisAlaGlnLeuArgAspLeuThrSerSerSerSerAspGluLeuSerTrp 138
 Db 534 GAGTACCTGTACTTCATCTCCACAGACATCCGCACA----- 569
 Qy 139 IleIleGluLeuLeuGluLysAspGlyMetAlaPheGlnGluAlaLeuAspProGlyPro 158
 Db 569 ----- 569
 Qy 159 PheapngllyserProPhealaglIngluleuAaspGlyglInglInalaserPro 178
 Db 570 -----CAAGTTACTCTTTTAAATGACCGCTGAAGAAAGCAAGCCACCATCAAGAC 623
 Qy 179 TyrHisProGlyserCyGlyAlaGlyAlaProSerProGlySerSerAspValSerThr 198
 Db 624 TATCGTATTCACACTGC-----TTGAANAACA 650
 Qy 199 AlaGlyThrGlyAlaSerArgSerSerHisSerSerAspSerGlyGlySerAspValasp 218
 Db 651 AGTGCATC--AAAGTCAGACTGTACAGT----- 680
 Qy 219 LeuAspProThrAspGlyLysLeuPheProSerAspGlyPheArgAspCysLysGly 238
 Db 680 ----- 680
 Qy 239 AspProLysHisGlyLysArgLysArgGlyArgProArgLysLeuSerLysGlyTrp 258
 Db 680 ----- 680
 Qy 259 AspCysLeuGluGlyLysLysSerLysHisAlaProArgGlyThrHisLeuTrpGluPhe 278
 Db 681 -----CATAGTAGAACAAAGCCCTCCAAAGTTCTCATGTAGGAATTT 722
 Qy 279 IleArgAspIleLeuIleHisProGluLeuAsnGluGlyLeuMetLysTrpGluAsnArg 298

```

Db 723 GTACACAGACCTCTCTATCTCTCTGAGAAACCTGTGCTATCTGAAATGGAGATAG 782
Qy 229 HtsglgllyvalPheLysPheLeuArgSerGluAlaValAlaGlnLeuTrpGlyGlnLys 318
Db 783 GAACAAGGAATTTTGGGTGGTGAATCGAAGCCCTGGCAAAAGATGGGGAACAAAG 842
Qy 319 LysLysAsnSerAsnMetThrTyrGlnLysLeuSerArgAlaMetArgTyrTyrLys 338
Db 843 AAGAAAAATGACAGATAGATGATGAAAGTTGAGCAGAGCCCTGAGATACTACTATAA 902
Qy 339 ArgGluIleLeuGlnArgValAspGlyArgArgLeuValTyrLysPheGlyLysAsnSer 358
Db 903 ACAGGAATTTTGGAGCGGGTTGAC---CGAAGTTAGTGTACAAATTTGAAAAATGCA 959
Qy 359 SerGlyTrpLysGluGluGluVal 366
Db 960 CACGGGTGGCAGGAAGACAGCTA 983

```

RESULT 14

US-09-009-913-10
Sequence 10. Application US/09009913

Patent No. 6087485

GENERAL INFORMATION:

APPLICANT: Axy's Pharmaceuticals, Inc.

TITLE OF INVENTION: Asphma Related Genes

NUMBER OF SEQUENCES: 339

CORRESPONDENCE ADDRESS:

ADDRESSEE: Bozicevic & Reed, LLP

STREET: 285 Hamilton Ave, Suite 200

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/009,913

FILING DATE: 21-JAN-1998

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Sherwood, Pamela J

REGISTRATION NUMBER: 36,677

REFERENCE/DOCKET NUMBER: SEQ-4P

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-327-3231

TELEFAX: 650-327-3231

TELEX:

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 2498 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-09-009-913-10

Alignment Scores:

```

Pred. No.: 4.95e-32 Length: 2498
Score: 422.00 Matches: 90
Percent Similarity: 45.45% Conservative: 50
Best Local Similarity: 29.22% Mismatches: 70
Query Match: 21.31% Indels: 98
DB: 3 Gaps: 5

```

US-08-978-217-2 (1-371) x US-09-009-913-10 (1-2498)

```

Qy 59 TrpLeuGlyGluGlnProGlnPheTrpSerLysThrGlnValIleuAspTrpIleSerLys 78
Db 423 TGGACATCAGTCACCCCTGAATACGACCTAAGCCCATGTGTGGAGTGTCTCCAGTTC 482
Qy 79 GlnValGlnLysAsnLysTyrAspAlaSerAlaIleAspPheSerArgCysAspMetAsp 98
Db 483 TGCTGCGACCGATACCAATGGACCAATTCATCTCTCTGCACTTCAACATCAGT 542
Qy 99 GlnAlaThrLeuCysAsnCysAlaLeuGlnLysLeuValPheGlyProLeuGly 118
Db 543 GGCTCGACAGCTGTGACGATGACACAGAGAGTTCGTGAGGACGCTGCGCTGCGGC 602
Qy 119 AspGlnLeuH1sAlaGlnLeuArgAspLeuThrSerSerSerSerAspGluLeuSerTrp 138
Db 603 GAGTACCTGTACTTCATCTCAGAACATCCGACCA----- 638
Qy 139 IleIleGlnLeuLeuGlnLysAspGlyMetAlaPheGlnGlnAlaLeuAspProGlyPro 158
Db 638 ----- 638
Qy 159 PheAspGlnGlySerProPheAlaGlnGlnLeuLeuAspAspGlyGlnGlnAlaSerPro 178
Db 639 -----CAAGTTACTCTTTTATATGACCGCTGAGAAAGCAAGCCACCATCAAGAC 692
Qy 179 TyrHisProGlySerCysGlyAlaGlyAlaProSerProGlySerSerAspValSerThr 198
Db 693 TATGCTGATTCACACTGC-----TTGAAAACA 719
Qy 199 AlaGlyThrGlnAlaSerArgSerHisSerSerAspSerGlyGlySerAspValAsp 218
Db 720 AGTGGCATT-----AAAAGTCAAGACTGTCAAGT----- 749
Qy 219 LeuAspProThrAspGlyLysLeuPheProSerAspGlyPheArgAspCysLysLysGly 238
Db 749 ----- 749
Qy 239 AspProLysHisGlyLysArgLysArgGlyArgProArgLysLeuSerLysGlyTrpTrp 258
Db 749 ----- 749
Qy 259 AspCysLeuGlnGlyLysLysSerLysHisAlaProArgGlyThrHisLeuTrpGluPhe 278
Db 750 -----CATGTAGAACAAAGCCCTCCAAAGTTCTCATCTATGGGAATTT 791
Qy 279 IleArgAspIleLeuIleHisProGluLeuAsnGlnGlyLeuMetLysTrpGluAsnArg 298
Db 792 GTACAGACGCTCTCTATCTCTCTGAGAAACCTGTGCAATTTCTGGAATGGGAAGATAG 851
Qy 299 HtsglgllyvalPheLysPheLeuArgSerGluAlaValAlaGlnLeuTrpGlyGlnLys 318
Db 852 GAACAAGGAATTTTCCGGTGGTGAATCGAAGCCCTGGCAAAAGATGTGGGACAAAG 911
Qy 319 LysLysAsnSerAsnMetThrTyrGlnLysLeuSerArgAlaMetArgTyrTyrLys 338
Db 912 AAGAAAAATGACAGATAGATGATGAAAGTTGAGCAGAGCCCTGAGATACTACTATAA 971
Qy 339 ArgGluIleLeuGlnArgValAspGlyArgArgLeuValTyrLysPheGlyLysAsnSer 358
Db 972 ACAGGAATTTTGGAGCGGGTTGAC---CGAAGTTAGTGTACAAATTTGAAAAATGCA 1028
Qy 359 SerGlyTrpLysGluGluGluVal 366
Db 1029 CACGGGTGGCAGGAAGACAGCTA 1052

```

RESULT 15

```

US-08-368-281-1
Sequence 1, Application US/08368281
Patent No. 5721113
GENERAL INFORMATION:
APPLICANT: Libermann, Towia A
APPLICANT: Oetegen, Joerg P
APPLICANT: Kunesh, Charles A
TITLE OF INVENTION: NERF Genes

```

NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SmithKline Beecham Corporation
 STREET: 709 Swedeland Road
 CITY: King of Prussia
 STATE: Pennsylvania
 COUNTRY: USA
 ZIP: 19406
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/368,281
 FILING DATE:
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Baumeister, Kirk
 REGISTRATION NUMBER: 33,833
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 610-270-5096
 TELEFAX: 610-270-5090
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2975 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-08-368-281-1

Alignment Scores:

Pred. No.:	1,41e-14	Length:	2975
Score:	246.50	Matches:	74
Percent Similarity:	40.43%	Conservative:	40
Best Local Similarity:	26.24%	Mismatches:	78
Query Match:	12.45%	Indels:	90
DB:	1	Gaps:	9

US-08-978-217-2 (1-371) x US-08-368-281-1 (1-2975)

QY 139 ILeIleGluLeuGluLysAspGlyMetAlaPheGlnGluAlaLeuAspProGlyPro 158
 Db 1 GTGGTAGTGTGTGCGGTGCGACGGCGGTGTCGCCGCCGCGGTGCCGCTCTCC 60
 QY 159 PheAspGlnGlySerProPheAlaGlnGluLeuAspAspGlyGlnGlnAlaSerPro 178
 Db 61 CTG-----CCGCCGCTGCTCAGCGGTGAAGTGAAGCAGAGCTCCAGCCC 111
 QY 179 -----TyrHisProGlySerCysGlyAla 186
 Db 112 CGGATTAACATGCGCAGCTTCTGCATGAGGACCCACGAACA-----GCT 159
 QY 187 G1yAlaProSerProGlySerSerAspValSerThr----- 198
 Db 160 GGATCTGTCTATCCGGCCGCGGAAGCATCACTTCACAGCAGTAAATGACACTGTACAGA 219
 QY 199 -----AlaGlyThrGlyAlaSer----- 204
 Db 220 TAAGACAATTGAAGCTGTAAGCCCTGTCATATGGAATCTCTACCTGCTTGAGGA 279
 QY 205 -----ArgSerSerHisSerSerAsp 211
 Db 280 TTCAAGAGTCTGAATTCATCATGCTGATGAGGCCAGATGTCAATTAAGAAACTGT 339
 QY 212 SerGlyGly-SerAspValAspLeuAspProThrAspGlyLysLeuPheProSer----- 229
 Db 340 AGTGAAGTGTCACTGAAGAGTCTGAAGCCATGATACCTCTCTATTCACACTCAC 399
 QY 230 -AspGlyPheArgAspCysLysLys----- 237
 Db 400 AGATAGCCATGAACCAATGAAGAAAAAGTTGGCCGTAACCAAGACCCAGCAATC 459

QY 238 -----GlyAspProLysHisGlyLysArgLysArgGlyArgProArgLysLe 253
 Db 460 ACCAATTTCCAAATGGGCTCTCTGAGTTAGGTATTAAGAAACCAAGA----- 508
 QY 253 uSerLysGluTyrTrpAspCysLeuGluGlyLysSerLysHisAlaProArgGlyTh 273
 Db 509 -----GAAAGAAAAGAAACACA-----AC 528
 QY 273 rHisLeuTrpGluPheIleArgAspIleLeuIleHisProGluLeuAsnGluGlyLeuMe 293
 Db 529 CTATTTGTGGAGTTCTTTTATGATCTACTTCAAGATAAAAATACTTGTCCAGGTATAT 588
 QY 293 LysTrpGluAsnArgHisGlyGlyValPheLysPheLeuArgSerGluAlaValAlaG 313
 Db 589 TAAATGACTCAGAGAGAAAAGGACATATTCAGCTGTGATTCAAAGGCTGTCTAA 648
 QY 313 nLeuTrpGlyGlnLysLysLysSerAsnMetThrTyrGluLysLeuSerArgAlaMe 333
 Db 649 GCTTTGGGAAAGCATTAAGAACAAACCAACATGAACTATGAAACCATGGAGCGAGCTTT 708
 QY 333 LArgTyrTyrLysArgGluIleLeuGluArgValAspGlyArgArgLeuValTyrLys 353
 Db 709 GAGTACTACTTACCAAGGGAATTTTGCAAAAGTTGAAGACAGAGCTTGTATATCA 768
 QY 353 sPhe 354
 Db 769 GTTC 772

Search completed: March 15, 2003, 23:32:40
 Job time : 94.0238 secs

